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Cellular and Molecular Life Sciences

MULTI-AUTHOR REVIEW

Selected aspects of the human gut microbiota

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Abstract The gut microbiota represents a highly complex assembly of microbes, which interact with each other and with their host. These interactions have various implications in terms of health and disease, and this multi-author review issue will address a number of selected aspects pertaining to gut microbiota research.

Keywords Microbiota · Microbiome · Probiotic · Gut commensals · Diet & health

Human beings are colonized by complex microbial communities that influence and govern various biological processes during their entire lifespan. Within the human body, microbes reach their highest density in the intestinal tract, where they form a complex microbial community known as the gut microbiota [1]. This gut microbiota develops during infancy of the host to reach its mature form following weaning [2–4]. The human gut microbiota in the early stages of life plays a pivotal role in the maturation and modulation of the host immune system, as well as in promoting various physiological processes in the human gut, such as the establishment of mucosal integrity and the mucus gel layer [5, 6].

Furthermore, later in life the abundance and prevalence of particular members of the human gut microbiota continue to play a variety of roles in the maintenance of human health, for example, by (i) assisting in the breakdown of food components and liberation of nutrients that would otherwise be inaccessible to the host, (ii) promoting the differentiation of particular host tissues, (iii) reducing the risk of gut colonization by pathogens, and (iv), as already mentioned above, maturation and modulation of the immune system. As underlined by several studies, the development of the complex microbial assemblage within a specific ecological niche reaches a so-called climax status represented by the establishment of a balanced equilibrium of its microbial components [7]. Numerous factors are known to cause shifts in the composition of the microbiota, thereby disrupting this microbial homeostasis and causing a state of dysbiosis. Dysbiosis is typically associated with having a negative impact on host health with long-term consequences, being associated with various disorders or diseases, such as obesity, diabetes, inflammatory bowel disease (IBD), and metabolic syndrome.

However, despite the wealth of publications that support the key roles played by gut microbiota in host health maintenance and promotion, there are still substantial knowledge gaps related to the associated mechanisms of action. Another intriguing finding of the metagenomic era is represented by the identification of numerous, but as yet uncharacterized microbial taxa that have overwhelmed bacterial taxonomy. Such newly discovered taxa represent a challenging frontier for microbiology research that focuses on the development of methodologies for the isolation and cultivation of these novel microbes.

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This multi-author review will cover a variety of topics, including the development of the gut microbiota following birth and the impact of antibiotics either prenatally or postnatally on these early microbial communities (see Nogacka et al.). In the context of early life microbiota, one particular group of gut commensals, the bifidobacteria, represents a dominant and prevalent microbial group. The contribution by Turroni et al. provides an overview of the ecological and biological role of bifidobacteria in the infant gut.

The multi-author review is counter-balanced by three articles focusing on gut microbiota composition in aging organisms, from flies to humans. The contribution by Clark and Walker presents a detailed overview of the role of gut microbiota in age-associated health decline as determined by the use of invertebrate models. In addition, in this context, the contribution by O'Toole and Jefferey provides insights into the composition of the gut microbiota of elderly, with particular emphasis on the role of microbial effector metabolites in host-signaling and impact on host health status. The contribution by Santoro et al. documents our current knowledge on gut microbiota composition at the extreme end of human life, namely in centenarians, providing relevant findings on the role of gut microbiota in neurodegenerative diseases, such as Parkinson's and Alzheimer's diseases.

Finally, comparative analysis of gut commensals found in two different mammalian species, humans and mice, revealed that they had a relatively small number of microorganisms in common (Hugenholtz and de Vos), and reminds us that extreme caution should be taken when findings from murine analyses are being extrapolated to humans.

Author contributions (1) Early microbiota, antibiotics and health. Alicja M. Nogacka, Nuria Salazar, Silvia Arboleya, Marta Suárez, Nuria Fernández, Gonzalo Solís, Clara G. de los Reyes-Gavilán, and Miguel Gueimonde. (2) Role of gut microbiota in aging-related health decline; insights from invertebrate models. Rebecca I. Clark and David W. Walker. (3) Bifidobacteria and the infant gut: an example of co-evolution and natural selection. Francesca Turroni, Christian Milani, Sabrina Duranti, Chiara Ferrario, Gabriele Andrea Lugli, Leonardo Mancabelli, Douwe van Sinderen, and Marco Ventura. (4) Microbiome–health interactions in older people. Paul O'Toole and Ian B. Jeffery. (5) Gut microbiota changes in the extreme decades of human life: a focus on centenarians. Aurelia Santoro, Rita Ostan, Marco Candela, Elena Biagi, Patrizia Brigidi, Miriam Capri, and Claudio Franceschi. (6) Mouse models for human intestinal microbiota research: a critical evaluation. Floor Hugenholtz and Willem M de Vos.

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